

AMENDMENT TO THE CLAIMS

WHAT IS CLAIMED IS:

1-11. (canceled)

12. (currently amended) A method of ~~analyzing cancer diseases~~ diagnosing breast cancer using a proteome image mining tool, comprising the steps of:

transforming inputted serum proteomes from normal individuals and individuals having breast cancer into two-dimensional images, extracting feature data from the images, generating a proteome standard by computing optimal features from the feature data, and constructing a database consisting of the proteome standard (Step 1);

inputting a serum proteome from a subject of interest, transforming the serum proteome into a two-dimensional image and extracting feature data from the image (Step 2); and

comparing the structure of the serum proteome pattern of the subject with the proteome standard and determining whether the serum proteome of the subject is normal or ~~abnormal~~, ~~that is~~, indicative of said subject having breast cancer (Step 3), wherein the proteome standard is one or more proteins selected from the group consisting of the spots listed in Table 1; and diagnosing said subject with breast cancer when said proteome is indicative of said subject having breast cancer.

13-14. (canceled)

15. (currently amended) The method ~~as set forth in any of claims 12 to 14~~ claim 12, wherein the Step 1 further includes the steps of extracting correlations between spots contained in the serum proteome from the two-dimensional images of the serum proteome employing experimental knowledge and a statistical method, and classifying the extracted correlations by a statistical method.

16. (canceled)

17. (currently amended) The method ~~as set forth in any of claims 12 to 14~~ claim 12, wherein the Step 3 of identifying the existence (~~development~~) of breast cancer includes:

a pattern matching step of classifying the serum proteome of the subject into ~~“normal” or “having a disease”~~ normal or having breast cancer by applying features and estimation functions, extracted upon producing the proteome standard, to the serum proteome of the subject; and

a fine classification step of deducing fine information including correlations between spots, contained in the two-dimensional proteome images.

18. (currently amended) The method ~~as set forth in any of claims 12 to 14~~ claim 12, further comprising a step of constructing a database consisting of the serum proteome of the subject and analysis results thereof, wherein said step is performed after the Step 3.

19. (currently amended) The method ~~as set forth in any of claims 12 to 14~~ claim 12, wherein the Step 1 of producing a proteome standard comprises:

a pre-processing step including an image processing step of performing noise filtering, image enhancement, ortho-projection and edge detection from the two-dimensional proteome images, and a feature extraction step of extracting basic features in spot form the image-processed two-dimensional images and producing feature data by labeling each of the extracted features; and

an evolutionary classification step of performing a genetic algorithm to discriminate optimal features playing a critical role in classification among the feature data extracted at the pre-processing step, and extracting optimal feature data and estimation functions by estimating fidelity of the optimal feature data discriminated by the genetic algorithm by a support vector machine using estimation functions and classification error rates.

20. (original) The method as set forth in claim 19, wherein the Step 1 of producing a proteome standard further comprises:

a fuzzy data mapping step of computing correlations between spots from the two-dimensional images of serum proteomes obtained at the pre-processing step, and classifying the computed features by a statistical method, and quantifying statistical inaccuracy using a fuzzy technique; and

a rule-based classification step of arranging and normalizing the results obtained at the data mapping step, and thus generating a final rule base.

21-22. (canceled)